```
Glu Ser Pro Arg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala
225                 230                 235                 240
Arg Lys Ser Leu Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val
                245                 250                 255
Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro
            260                 265                 270
Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu
        275                 280                 285
Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn
    290                 295                 300
Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly
305                 310                 315                 320
Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe
                325                 330                 335
Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu
            340                 345                 350
His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr
        355                 360                 365
Val Ala Leu Leu Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser
    370                 375                 380
Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly
385                 390                 395                 400
Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
                405                 410                 415
Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
            420                 425                 430
Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr
        435                 440                 445
Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr
    450                 455                 460
Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser
465                 470                 475                 480
Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro
                485                 490                 495
Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp
            500                 505
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Glu Gln Gln Asp Gln Ser Met Lys Glu Gly Arg Leu Thr Leu Val
  1                 5                  10                  15
Leu Ala Leu Ala Thr Leu Ile Ala Ala Phe Gly Ser Ser Phe Gln Tyr
            20                  25                  30
Gly Tyr Asn Val Ala Ala Val Asn Ser Pro Ala Leu Leu Met Gln Gln
        35                  40                  45
Phe Tyr Asn Glu Thr Tyr Tyr Gly Arg Thr Gly Glu Phe Met Glu Asp
    50                  55                  60
Phe Pro Leu Thr Leu Leu Trp Ser Val Thr Val Ser Met Phe Pro Phe
65                  70                  75                  80
Gly Gly Phe Ile Gly Ser Leu Leu Val Gly Pro Leu Val Asn Lys Phe
                85                  90                  95
Gly Arg Lys Gly Ala Leu Leu Phe Asn Asn Ile Phe Ser Ile Val Pro
            100                 105                 110
```

```
Ala Ile Leu Met Gly Cys Ser Arg Val Ala Thr Ser Phe Glu Leu Ile
        115                 120                 125
Ile Ile Ser Arg Leu Leu Val Gly Ile Cys Ala Gly Val Ser Ser Asn
    130                 135                 140
Val Val Pro Met Tyr Leu Gly Glu Leu Ala Pro Lys Asn Leu Arg Gly
145                 150                 155                 160
Ala Leu Gly Val Val Pro Gln Leu Phe Ile Thr Val Gly Ile Leu Val
                165                 170                 175
Ala Gln Ile Phe Gly Leu Arg Asn Leu Leu Ala Asn Val Asp Gly Trp
            180                 185                 190
Pro Ile Leu Leu Gly Leu Thr Gly Val Pro Ala Ala Leu Gln Leu Leu
        195                 200                 205
Leu Leu Pro Phe Phe Pro Glu Ser Pro Arg Tyr Leu Leu Ile Gln Lys
    210                 215                 220
Lys Asp Glu Ala Ala Ala Lys Lys Ala Leu Gln Thr Leu Arg Gly Trp
225                 230                 235                 240
Asp Ser Val Asp Arg Glu Val Ala Glu Ile Arg Gln Glu Asp Glu Ala
                245                 250                 255
Glu Lys Ala Ala Gly Phe Ile Ser Val Leu Lys Leu Phe Arg Met Arg
            260                 265                 270
Ser Leu Arg Trp Gln Leu Leu Ser Ile Ile Val Leu Met Gly Gly Gln
        275                 280                 285
Gln Leu Ser Gly Val Asn Ala Ile Tyr Tyr Tyr Ala Asp Gln Ile Tyr
    290                 295                 300
Leu Ser Ala Gly Val Pro Glu Glu His Val Gln Tyr Val Thr Ala Gly
305                 310                 315                 320
Thr Gly Ala Val Asn Val Val Met Thr Phe Cys Ala Val Phe Val Val
                325                 330                 335
Glu Leu Leu Gly Arg Arg Leu Leu Leu Leu Leu Gly Phe Ser Ile Cys
            340                 345                 350
Leu Ile Ala Cys Cys Val Leu Thr Ala Ala Leu Ala Leu Gln Asp Thr
        355                 360                 365
Val Ser Trp Met Pro Tyr Ile Ser Ile Val Cys Val Ile Ser Tyr Val
    370                 375                 380
Ile Gly His Ala Leu Gly Pro Ser Pro Ile Pro Ala Leu Leu Ile Thr
385                 390                 395                 400
Ile Phe Leu Gln Ser Ser Arg Pro Ser Ala Phe Met Val Gly Gly Ser
                405                 410                 415
Val His Trp Leu Ser Asn Phe Thr Val Gly Leu Ile Phe Pro Phe Ile
            420                 425                 430
Gln Glu Gly Leu Gly Pro Tyr Ser Phe Ile Val Phe Ala Val Ile Cys
        435                 440                 445
Leu Ile Thr Thr Ile Tyr Ile Phe Leu Ile Val Pro Glu Thr Lys Ala
    450                 455                 460
Lys Thr Phe Ile Glu Ile Asn Gln Ile Phe Thr Lys Met Asn Lys Val
465                 470                 475                 480
Ser Glu Val Tyr Pro Glu Lys Glu Glu Leu Lys Glu Leu Pro Pro Val
                485                 490                 495
Thr Ser Glu Gln
            500
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTTTCCTAG TCTTTGCTAC A 21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGTTAAGGC CTTCCATT 18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Xaa Xaa Gly Phe Gln Xaa Gly Ser Val Thr Gly Thr Leu Val Leu
  1               5                  10                  15
Ala Val Leu Ile Ala Ala Leu Gly Ser Phe Gln Tyr Gly Tyr Asn Leu
            20                  25                  30
Gly Val Ile Asn Ala Pro Gln Lys Val Ile Glu Ala Phe Tyr Glu Thr
        35                  40                  45
Trp Leu Gly Arg Xaa Gly Glu Xaa Pro Ser Val Pro Thr Leu Thr Leu
    50                  55                  60
Leu Trp Ser Leu Ser Val Ser Ile Phe Ala Val Gly Gly Met Ile Gly
65                  70                  75                  80
Ser Phe Leu Val Gly Xaa Ile Gly Asn Arg Leu Gly Arg Lys Xaa Ala
                85                  90                  95
Met Leu Val Asn Asn Val Leu Ala Ile Ala Gly Gly Leu Leu Met Gly
            100                 105                 110
Leu Ala Lys Xaa Ala Xaa Ser Phe Glu Met Leu Ile Leu Gly Arg Phe
        115                 120                 125
Ile Ile Gly Leu Tyr Cys Gly Leu Ser Ser Gly Val Val Pro Met Tyr
    130                 135                 140
Val Gly Glu Ile Ser Pro Thr Ala Leu Arg Gly Ala Leu Gly Thr Leu
145                 150                 155                 160
Asn Gln Leu Gly Ile Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly
                165                 170                 175
Leu Asp Ser Leu Leu Gly Asn Glu Ser Leu Trp Pro Leu Leu Leu Gly
            180                 185                 190
Leu Thr Gly Val Pro Ala Leu Leu Gln Leu Leu Leu Leu Pro Phe Cys
        195                 200                 205
Pro Glu Ser Pro Arg Tyr Leu Leu Ile Asn Lys Asn Glu Glu Ala Arg
    210                 215                 220
Ala Lys Lys Ala Leu Gln Arg Leu Arg Gly Thr Ala Asp Val Ser Gln
225                 230                 235                 240
Glu Val Ala Glu Met Lys Asp Glu Ser Arg Xaa Met Xaa Ser Glu Lys
                245                 250                 255
```